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General Physiology is the study of biological mechanisms through analytical investigations, which decipher the molecular and cellular mechanisms underlying biological function at all levels of organization.

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EDITORIALS

1 The legacy of Olaf Sparre Andersen and future directions of the *Journal of General Physiology*. Edward N. Pugh Jr.

COMMENTARIES

5 PIP_2 PIP_2 hooray for maxi K^+. Ann R. Rittenhouse

9 Fusion gains independence. Manfred Lindau

ARTICLES

13 Direct regulation of BK channels by phosphatidylinositol 4,5-bisphosphate as a novel signaling pathway. Thirumalini Vaithianathan, Anna Bukiya, Jianxi Liu, Penchong Liu, Maria Asuncion-Chin, Zheng Fan, and Alejandro Dopico

29 Massive Ca-induced membrane fusion and phospholipid changes triggered by reverse Na/Ca exchange in BHK fibroblasts. Alp Yaradanakul, Tzu-Ming Wang, Vincenzo Lariccia, Mei-Jung Lin, Chengcheng Shen, Xinran Liu, and Donald W. Hilgemann

51 Ca-dependent nonsecretory vesicle fusion in a secretory cell. Tzu-Ming Wang and Donald W. Hilgemann

67 Mechanosensitive channel MscS in the open state: modeling of the transition, explicit simulations, and experimental measurements of conductance. Andriy Anishkin, Kishore Kamaraju, and Sergei Sukharev

85 Amino acid substitutions in the pore helix of GluR6 control inhibition by membrane fatty acids. Timothy J. Wilding, Elisabeth Fulling, Yun Zhou, and James E. Huettner

101 Differential interactions of Na^+ channel toxins with T-type Ca^{2+} channels. Hui Sun, Diego Varela, Denis Chartier, Peter C. Ruben, Stanley Nattel, Gerald W. Zamponi, and Normand Leblanc

115 Species-specific differences among KCNMB3 BK β3 auxiliary subunits: some β3 N-terminal variants may be primate-specific subunits. Xuhui Zeng, Xiao-Ming Xia, and Christopher J. Lingle

131 How ATP inhibits the open K_{ATP} channel. Tim J. Craig, Frances M. Ashcroft, and Peter Proks

145 A close association of RyRs with highly dense clusters of Ca^{2+}-activated Cl^- channels underlies the activation of STICs by Ca^{2+} sparks in mouse airway smooth muscle. Rongfeng Bao, Lawrence M. Lifshitz, Richard A. Tuft, Karl Bellvé, Kevin E. Fogarty, and Ronghua ZhuGe

161 HCO_3^- secretion by murine nasal submucosal gland serous acinar cells during Ca^{2+}-stimulated fluid secretion. Robert J. Lee, Janice M. Harlow, Maria P. Limberis, James M. Wilson, and J. Kevin Foskett

185 Intracellular proton regulation of ClC-0. Giovanni Zifarelli, Anna Rosa Murgia, Paolo Soliani, and Michael Pusch

1a Abstracts of papers at the Sixty-Second Annual Meeting of the Society of General Physiologists

29a Index to authors of abstracts

Cover picture: The transmembrane domain of the bacterial mechanosensitive channel MscS in MD-equilibrated closed (left panel) and open (center) states. In the closed state, the gate (yellow) is dehydrated; in the open state, which is 10 Å wider, the pore is hydrated and conductive. The hydration energy profiles are shown on the right (see article by Anishkin et al., 67–83).

JGP

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ARTICLES

199 **$Na_v1.4$ deregulation in dystrophic skeletal muscle leads to Na^+ overload and enhanced cell death.** Carole Hirn, George Shapovalov, Olivier Petermann, Emmanuelle Roulet, and Urs T. Ruegg

209 **Voltage clamp fluorimetry reveals a novel outer pore instability in a mammalian voltage-gated potassium channel.** Moninder Vaid, Thomas W. Claydon, Saman Rezazadeh, and David Fedida

223 **Permeation and gating in $Ca_V3.1$ (α1G) T-type calcium channels effects of Ca^{2+}, Ba^{2+}, Mg^{2+}, and Na^+.** Nilofar Khan, I. Patrick Gray, Carlos A. Obejero-Paz, and Stephen W. Jones

239 **Ni^{2+} block of $Ca_V3.1$ (α1G) T-type calcium channels.** Carlos A. Obejero-Paz, I. Patrick Gray, and Stephen W. Jones

251 **α-Scorpion toxin impairs a conformational change that leads to fast inactivation of muscle sodium channels.** Fabiana V. Campos, Baron Chanda, Paulo S.L. Beirão, and Francisco Bezanilla

265 **Nicotinic receptor interloop proline anchors β1-β2 and cys loops in coupling agonist binding to channel gating.** Won Yong Lee, Chris R. Free, and Steven M. Sine

279 **ACTH inhibits bTREK-1 K^+ channels through multiple cAMP-dependent signaling pathways.** Haiyan Liu, Judith A. Enyeart, and John J. Enyeart

TUTORIAL RESEARCH ARTICLES

295 **Linking exponential components to kinetic states in markov models for single-channel gating.** Christopher Shelley and Karl L. Magleby

LETTERS TO THE EDITOR

313 **A comment on ion channels as pharmacological targets in oncology.** Andrea Becchetti and Annarosa Arcangeli

Cover picture: Absense of dystrophin in skeletal muscle cells causes disruption in localization and kinetic properties of Nav1.4 ion channels. (Top) Images of Nav1.4 immunofluorescence in single C57BL/6J (left) and mdx5cv (right) fibers show disruption in a longitudinally striated pattern in mdx. (Bottom) Representative traces of cell-attached Na^+ currents in control (left) and mdx (right) fibers show increased activity and prolonged inactivation in mdx cells (see article by Hirn et al., 199–208).

JGP

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ARTICLES

315 **Divalent cations regulate connexin hemichannels by modulating intrinsic voltage-dependent gating.** Vytas K. Verselis and Miduturu Srinivas

329 **Glucose and GLP-1 stimulate cAMP production via distinct adenylyl cyclases in INS-1E insulinoma cells.** Lavoisier S. Ramos, Jonathan Hale Zippin, Margarita Kamenetsky, Jochen Buck, and Lonny R. Levin

339 **Nitric oxide–mediated modulation of synaptic activity by astrocytic P2Y receptors.** Bhupesh Mehta, Gulnaz Begum, Nanda B. Joshi, and Preeti G. Joshi

351 **Preventing voltage-dependent gating of anthrax toxin channels using engineered disulfides.** Damon S. Anderson and Robert O. Blaustein

361 **A carboxy-terminal inter-helix linker as the site of phosphatidylinositol 4,5-bisphosphate action on Kv7 (M-type) K^+ channels.** Ciria C. Hernandez, Oleg Zaika, and Mark S. Shapiro

383 **Mutations of nonconserved residues within the calcium channel α_1-interaction domain inhibit β-subunit potentiation.** Giovanni Gonzalez-Gutierrez, Erick Miranda-Laferte, David Naranjo, Patricia Hidalgo, and Alan Neely

Cover picture: Effects of site-directed mutagenesis of the carboxy-terminal A-B inter-helix linker of Kv7.2 channels on single-channel open probability correlate with docking simulations of a PIP_2 analog. Recordings of R463Q (top) or R463E (bottom) mutants at 0 mV in cell-attached mode (left) or inside-out mode in the presence of 25 μM diC8-PIP_2 (right). The simulations below the traces predict a much more favorable interaction for the R463E mutant (see article by Hernandez et al., 361–381).

JGP

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ARTICLES

397 **Excitation–contraction coupling of the mouse embryonic cardiomyocyte.** Risto Rapila, Topi Korhonen, and Pasi Tavi

407 **Mathematical model of mouse embryonic cardiomyocyte excitation–contraction coupling.** Topi Korhonen, Risto Rapila, and Pasi Tavi

421 **ATP inhibition of CLC-1 is controlled by oxidation and reduction.** Xiao-Dong Zhang, Pang-Yen Tseng, and Tsung-Yu Chen

429 **Luminal Mg^{2+}, a key factor controlling RYR2-mediated Ca^{2+} release: cytoplasmic and luminal regulation modeled in a tetrameric channel.** Derek R. Laver and Bonny N. Honen

447 **Gating pore currents in DIIS4 mutations of NaV1.4 associated with periodic paralysis: saturation of ion flux and implications for disease pathogenesis**. Arie F. Struyk, Vladislav S. Markin, David Francis, and Stephen C. Cannon

465 **Steady-state function of the ubiquitous mammalian Na/H exchanger (NHE1) in relation to dimer coupling models with 2Na/2H stoichiometry.** Daniel Fuster, Orson W. Moe, and Donald W. Hilgemann

Cover picture: Laser scanning confocal image from a fluo-4–loaded, isolated E10 spontaneously active cardiomyocyte (left) with corresponding line-scan (yellow line) through the cytosol surrounding the nucleus (red n). Graphs above the line-scan image show relative calcium signals from near–sarcoplasmic reticulum (red line) and near-sarcolemma (blue line). Inset (gray background) shows both graphs in an expanded timescale from selected area below (gray; see article by Rapila et al., 397–405).

JGP

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BRIEF REVIEWS

481 **Multiple unbiased prospective screens Identify TRP channels and their conserved gating elements.** Benjamin R. Myers, Yoshiro Saimi, David Julius, and Ching Kung

COMMENTARIES

487 **Return of the electric binding site.** Brad S. Rothberg

ARTICLES

491 **Measurements of the BK_{Ca} channel's high-affinity Ca^{2+} binding constants: effects of membrane voltage.** Tara-Beth Sweet and Daniel H. Cox

507 **hERG gating microdomains defined by S6 mutagenesis and molecular modeling.** Sarah L. Wynia-Smith, Anne Lynn Gillian-Daniel, Kenneth A. Satyshur, and Gail A. Robertson

521 **ENaC proteolytic regulation by channel-activating protease 2.** Agustín García-Caballero, Yan Dang, Hong He, and M. Jackson Stutts

537 **Rescue of volume-regulated anion current by bestrophin mutants with altered charge selectivity.** Li-Ting Chien and H. Criss Hartzell

547 **Properties of the Inner pore region of TRPV1 channels revealed by block with quaternary ammoniums.** Andrés Jara-Oseguera, Itzel Llorente, Tamara Rosenbaum, and León D. Islas

563 **The $P2X_7$ receptor channel pore dilates under physiological Ion conditions.** Zonghe Yan, Shuo Li, Zhaodong Liang, Melanija Tomić, and Stanko S. Stojilkovic

575 **Contribution of the myosin binding protein c motif to functional effects in permeabilized rat trabeculae.** Maria V. Razumova, Kristina L. Bezold, An-Yue Tu, Michael Regnier, and Samantha P. Harris

587 **Kinetics of turn-offs of frog rod phototransduction cascade.** Luba A. Astakhova, Michael L. Firsov, and Victor I. Govardovskii

Cover picture: S6 mutations causing constitutive activation of hERG channels. The mutant channels are conductive at negative potentials (top left), their tail currents fail to decay to baseline (middle left) and have slower time constants (bottom left). Four energy-minimized models with open (top) and closed (bottom) states viewed laterally (left) and from the cytosol (right). In the closed state, Y667 and S668 from adjacent subunits make contact, forming a ring from which the Q664 side chains extend toward the pore axis and occlude the pore (see article by Wynia-Smith et al., 507–520).

JGP

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MILESTONES IN PHYSIOLOGY

607 **The two-membrane model of epithelial transport: Koefoed-Johnsen and Ussing (1958).** Lawrence G. Palmer and Olaf S. Andersen

ARTICLES

613 **Long-pore electrostatics in inward-rectifier potassium channels.** Janice L. Robertson, Lawrence G. Palmer, and Benoît Roux

633 **Slow inactivation in *Shaker* K channels is delayed by intracellular tetraethylammonium.** Vivian González-Pérez, Alan Neely, Christian Tapia, Giovanni González-Gutiérrez, Gustavo Contreras, Patricio Orio, Verónica Lagos, Guillermo Rojas, Tania Estévez, Katherine Stack, and David Naranjo

651 **Molecular template for a voltage sensor in a novel K^+ channel. III. Functional reconstitution of a sensorless pore module from a prokaryotic Kv channel.** Jose S. Santos, Sergey M. Grigoriev, and Mauricio Montal

667 **Kv channel gating requires a compatible S4-S5 linker and bottom part of S6, constrained by non-interacting residues.** Alain J. Labro, Adam L. Raes, Alessandro Grottesi, Diane Van Hoorick, Mark S.P. Sansom, and Dirk J. Snyders

681 **Regulation of bestrophin Cl channels by calcium: Role of the c terminus.** Qinghuan Xiao, Andrew Prussia, Kuai Yu, Yuan-yuan Cui, and H. Criss Hartzell

693 **Identification of channel-lining amino acid residues in the hydrophobic segment of colicin Ia.** Paul K. Kienker, Karen S. Jakes, and Alan Finkelstein

709 **The roles of pore ring and plug in the SecY protein-conducting channel.** James Gumbart and Klaus Schulten

721 **Modulation of the local SR Ca^{2+} release by intracellular Mg^{2+} in cardiac myocytes.** Konstantin Gusev and Ernst Niggli

731 **Voltage dependence of ATP secretion in mammalian taste cells.** Roman A. Romanov, Olga A. Rogachevskaja, Alexander A. Khokhlov, and Stanislav S. Kolesnikov

Cover picture: Molecular dynamics model of the SecY channel in the membrane. Views highlighting the central pore ring (yellow surface) are shown in the middle and right panels. Simulations reveal that the ring is mainly responsible for closing SecY. Plugs in native and two mutated channels are shown in green, blue, and red, respectively; these stabilize ring closure, but do not seal the channel (see article by Gumbart and Schulten, 709–719).